

OM nucleic - nucleic search, using SW nucloc-  
 March 11, 2003, 03:27:47 ; Search time 490 Seconds  
 (without alignments) updates/sec  
 15322.780 Million cell

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Searched: 2185529 seqs
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Minimum Match 0%
Maximum Match 100%
Post-processing: Minimum Match 100%
                  Maximum Match 100%
                  Matching first 45 summaries
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Listing 11.10
Database :
N.Genesed.101002:*
1: /SID52/gcgdata/genesed/geneseqn-emb1/NA1981.DAT: *
1: /SID52/gcgdata/genesed/geneseqn-emb1/NA1982.DAT: *
1: /SID52/gcgdata/genesed/geneseqn-emb1/NA1983.DAT: *
1: /SID52/gcgdata/genesed/geneseqn-emb1/NA1980.DAT: *

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23: /SID52/5/gcgdata/genesec4/5  
24: /SID52/5/gcgdata/genesec4/5

## Description

Result No.	Score	Query Match	Length	DB	ID
1	3334	100.0	3334	22	AAE28030
2	3303.4	99.1	3280	21	AA621262
3	3259.6	97.8	3331	22	AA895442
4	3258.8	97.7	3233	22	AA889165
5	2726.6	81.8	2610	22	AAE89175
6	2603.6	78.1	2554	22	AAE77987
7	2527.4	75.8	1777	20	AAE21991
8	17105	51.1	1239	23	ABV3150
9	1172.8	35.2			

10	1172.8	35.2	1299	23	BAF89791
11	1145.8	34.4	1149	22	BAF87515
12	1008.8	30.3	1587	22	BAF75095
13	976.2	28.3	3356	22	BAF76196
14	951.8	27.5	1119	22	BAF75654
15	901.4	27.0	3390	22	BAF95443
16	65.4	19.2	677	21	BAF89776
17	65.4	18.8	627	22	BAF89199
18	551	16.5	625	21	BAF84270
19	545.8	16.4	558	22	BAF18491
20	537.6	16.4	686	22	BAF18281
21	464.6	13.9	1737	22	BAF40854
22	444	13.3	4477	20	BAF4107
23	443	12.7	466	20	BAF89165
24	424.4	12.6	426	24	BAF83875
25	419.8	11.0	1508	22	BAF84886
26	367.8	10.9	387	23	BAF40087
27	364	10.9	387	23	BAF44075
28	362.4	10.9	551	22	BAF20220
29	362.4	10.5	390	22	BAF11472
30	349.4	10.4	373	23	BAF114042
31	346.6	10.4	445	23	BAF35336
32	346.6	10.4	445	23	BAF35336
33	346.6	10.4	435	22	BAF49597
34	340.8	10.2	435	22	BAF49737
35	338	10.1	397	22	BAF11321
36	336.6	9.6	490	22	BAF11188
37	331.2	9.9	342	22	BAF27999
38	331.2	9.7	342	22	BAF28037
39	290	8.7	291	22	BAF28000
40	289	8.5	291	22	BAF28038
41	284.4	8.5	366	23	BAF59729
42	284.4	8.5	366	23	BAF59729
43	265	7.9	294	22	BAF80339
44	264	7.9	267	22	BAF28001
45					

## ALIGNMENTS

1	UT 1	
2	8030	
3	AAFE28030 standard; DNA; 3334 BP	
4	AAFE28030;	
5	08-MAY-2001 (first entry)	
6	Human TR13 receptor coding sequence SEQ ID NO: 39.	
7	Human TR13 receptor coding sequence SEQ ID NO: 39.	
8	Human: tumour necrosis factor receptor; TR13; TR14; infection;	
9	Human: autoimmune disease; allergy; inflammatory disease; ds	
10	cancer; rejection; apoptosis; cardiovascular disease; aneurysm; ds	
11	graft rejection; apoptosis; cardiovascular disease; aneurysm; ds	
12	Homo sapiens.	
13	WO200105834-A1.	
14	25-JAN-2001.	
15	14-JUL-2000; 2000WO-US19343.	
16	16-JUL-1999; 99US-0144487.	
17	18-AUG-1999; 99US-0149450.	
18	20-AUG-1999; 99US-0149712.	
19	10-SEP-1999; 99US-0153089.	
20	(HUMA-) HUMAN GENOME SCI INC.	
21	Ruben SM, Ni J, Young PE;	
22	WPI; 2001-112682/12.	

Human prostate exp  
Nucleotide sequenc  
Human seven-transam  
TR16-1 long receptor  
Human seven-transam  
TR16-shortB619 prot  
Human CASHB619 prot  
Nucleotide sequenc  
Human colon cancer  
Human polynucleoti  
Human breast cancer  
Human SEC10 nuclei  
Human secreted pro  
Human secreted a hu  
CDNA fragment lung  
CDNA encoding nucleic  
Human SEC5 cancer  
Human breast cancer  
Human prostate exp  
Human breast cancer  
Human breast cancer  
Human breast cancer  
Human breast exp  
Human prostate exp  
Human prostate exp  
Human prostate exp  
Human prostate cancer  
Human breast cancer  
Human TR13 coding  
Human TR13 coding  
Human TR13 coding  
Human TR13 coding  
CDNA #754 encoding  
Prostate cancer t  
Human TR13 coding  
Human TR13 coding

XX Nucleic acids encoding 2 human tumor necrosis factor receptor  
PP polypeptides (TR13) and (TR14), useful for the prevention, diagnosis  
PP and treatment of, e.g. cancers, acquired immune deficiency syndrome and  
XX hypohidrotic ectodermal dysplasia -  
PS Claim 4: Page 394-398; 418pp; English.  
XX The present invention provides the protein and coding sequences of the  
CC human tumor necrosis factor receptors TR13 and TR14. These sequences are  
CC useful in the diagnosis and treatment of many diseases, including cancer,  
CC autoimmune diseases, cardiovascular disorders, allergies, including cancer,  
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and  
XX infections.

Sequence 3334 BP: 820 A; 952 C; 811 G; 751 T; 0 other;  
Query Match Best Local Similarity 100.0%; Score 3334; DB 22; Length 3334;  
Matches 3334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAGGACGACGCGGACGACCTGAGCGGCTACTGCGCGCTGAGAGAGAGCTATG 60  
DB 1 GCAGAGGACGACGCGGACGACCTGAGCGGCTACTGCGCGCTGAGAGAGAGCTATG 60  
QY 61 GCTGAGCTGGGACAGGACGACCTATCTCCGACAGAGTGAAGGAGAGAGAGAGAG 60  
DB 61 GCTGAGCTGGGACAGGACGACCTATCTCCGACAGAGTGAAGGAGAGAGAGAGAG 60  
QY 121 ATACCCGCTGTGGGCGGCTGTGCTGTGGGCGGACCGGCTTCAGAGTGAAGAGAG 120  
DB 121 ATACCCGCTGTGGGCGGCTGTGCTGTGGGCGGACCGGCTTCAGAGTGAAGAGAG 120  
QY 181 ACAGGACGAGCTTACGCGCTGCAAGAGTGTGAGTACAGTGTGAGAGAGAGAG 180  
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QY 301 CTGCTGACCGGCTCAAGGAGGACGAGAGTGTGCTTCTGCTGAGAGAGAGAG 300  
DB 301 CTGCTGACCGGCTCAAGGAGGACGAGAGTGTGCTTCTGCTGAGAGAGAGAG 300  
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DB 421 ATTGAGTGTGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 420  
QY 481 GAGCTGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 480  
DB 481 GAGCTGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 480  
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DB 541 CGGAGGACGACGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 540  
QY 601 AACCTGAGAGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 600  
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QY 661 TTTGAGTGTGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 660  
DB 661 TTTGAGTGTGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 660  
QY 721 AAGAGCAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 720  
DB 721 AAGAGCAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 720  
QY 781 AAGAGCAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 780  
DB 781 AAGAGCAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 780

QY 781 CTCTATTGAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 780  
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QY 841 AGAAG 840  
DB 841 AGAAG 840  
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DB 901 AGAAG 900  
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DB 961 AATAG 960  
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DB 1741 AG 1740  
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DB 1801 AATGAG 1800  
QY 1861 TGACAG 1860  
DB 1861 TGACAG 1860

[illegible]

Db 2941 GCCATCATGGAGGCGAGATGTGAGAGCAGCACCCTATCTTTACCACGACGAAATCACTCT 3000  
 Oy 3001 TTGGGAAGATCAAAATCATTTTACCTCCACAGAGACCTCGATGTGATTTGACTCAGTCCGC 3060  
 Db 3001 TTGGGAATCAAAATCATTTTACCTCCAGAGACCTCGATGTGATTTGACTCAGTCCGC 3120  
 Oy 3061 TGAAGACATCCCGAGAGGCCACGACATGAGACCTGTGGAGAGCAGCTGCTGGCTCACCCTG 3180  
 Db 3061 TGAAGACATCCCGAGAGGCCACGACATGAGACCTGTGGAGAGCAGCTGCTGGCTCACCCTG 3180  
 Oy 3061 TGAAGACATCCCGAGAGGCCACGACATGAGACCTGTGGAGAGCAGCTGCTGGCTCACCCTG 3180  
 Db 3061 TGAAGACATCCCGAGAGGCCACGACATGAGACCTGTGGAGAGCAGCTGCTGGCTCACCCTG 3180  
 Oy 3121 CCTCTCATCTGCGATATACACCTTTTGCAAGCCTCGCGCATTTTGGGTGCCAGATCCTGC 3240  
 Db 3121 CCTCTCATCTGCGATATACACCTTTTGCAAGCCTCGCGCATTTTGGGTGCCAGATCCTGC 3240  
 Oy 3181 AACACCCACTGCTGGAATATCTCTTCATTTGTGGGCTTATACAGATTTGATTCAGATCT 3300  
 Db 3181 AACACCCACTGCTGGAATATCTCTTCATTTGTGGGCTTATACAGATTTGATTCAGATCT 3300  
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 Db 3301 CACTTGTGTAAATTAATAAAAAAAAAAAAAA 3334  
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 Db 3301 CACTTGTGTAAATTAATAAAAAAAAAAAAAA 3334

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WPI, 2001-408281/43.  
P-Psds; AAU2190.  
Gerritsen ME, Deforge L, Desnoyers L, Filvaroff E, Gao W, Smith V, Stewart TA, Tamas D, Matanabe CK, Wood WI, Zhang Z.

isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to detect lung, breast, prostate, and cervical - tumours e.g. Claim 3; Fig 37; 813pp; English.

CC PRO polypeptides encode for novel human secretory and transmembrane  
CC PRO polypeptides, to link bioactive molecules are useful to detect other  
CC PRO polypeptides, to modulate biological activities of cells expressing  
CC breast, prostate, and to detect biological activities of cells expressing  
CC polypeptide expression, rectal, cervical the presence of mammalian lung, colon,  
CC Some of the 275 sequences are also sample to that in a control sample.  
CC Tumour necrosis factor- $\alpha$  (TNF- $\alpha$ ) from stimulate the proliferation of  
CC Proliferation or factor- $\alpha$  (TNF- $\alpha$ ) from stimulate the proliferation of  
CC gene expression or differentiation of chondrocytes, the release of  
CC of fibrinogen, the proliferation of chondrocytes, the release of  
CC of T-lymphocytes, the proliferation of chondrocytes, the release of  
CC monocytes (PBMCs), or the release of inner ear utricular supporting cells  
CC the PRO polypeptide, or the proliferation of endothelial cells or  
CC to skeletal muscle cells may modulate glucose or the fatty acid uptake by  
CC to factor VIIA. The PRO polypeptides can inhibit binding of a peptide  
CC PRO polypeptides involved in binding interactions. The polynucleotides can  
CC transgenic or knock out animals and can be used in gene expression  
XX Sequence 3501 BP: 921 A; 979 G; 823 G; 776 T; 2 other:  
Query Match  
Best Local Similarity 99.1%; Score 30  
Matches

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    3541:  Conserved: 99.6%;  Preg No. 0;  DB 22;  Length 3501;
    Db 1  CGAAGACGACAGACCCGACACATCGATGACCGCTACTGCGCTACATCTAGGACAAAGCATAT
    76  GCGAAGACAGACAGACCGCGACGACCTGAGACCCGCTACTGACCGCTCTACCTAGAGAACAAAGCATAT
    Oy  61  GCTGAGCTGGGCGACACAGCACCATCTCTCTCGCCAGAGTCAAGGGGGAAGAACTGAGAGCGCC
    Db  136  GCGAGACCTGGGCGACACAGCACCATCTCTCTCGCCAGAGTCAAGGAAGAAACTGAGAGCGCC
    Oy  121  ATACCCCGGCGTGGGCGCTGCTGCTCTGGGCGGGAGCCGCTTCACAGGTGACCCAGG
    Db  196  ATACCCCGGCTGGGCGGCGCTCTCTCTCTGGGCGGGAGCCGCTTCACAGGTGACCCAGG
    Oy  181  ACGGAGCCGACACTTCAGACGCGCTGCGCAAAAGATCTAGTACACTATGATTAACGGGTGT
    Db  256  ACGGAGCCGACGACTTCATGCTCTGCGCAAAAGATCTGAGTACCACTATGATTAACAGCGGTGT
    Oy  241  GACGACGAGGCTTCAGATGAGGTGCGCGGTGCGCGCATACCCCGGGGCGCTGGACACGAG
    Db  316  GACACACAGGCTTCAGATGAGGTGCGCGGTGCGCGCATACCCCGGGGCGCTGGACACGAG
    Oy  301  CTGCGCTACCCCGTCAAGGGCAACCGAGTGTCTCTCTGCGCAAGCGCGGGAGATTCTG
    Db  376  CTGCTGACGACCCCGTCAAGGGCAACCGAGTGTCTCTCTGCGCAAGCGCGGGAGATTCTG
    Oy  361  GATATGAAGACACAGTCACTGTTAAGCATGGCGTGAAGGCGCGCTACTCCCTCGGACACAGC
  
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Page 4

[illegible][illegible]







XX MPI: 2001-328651/34.  
DR P-PSDB: AAB83845.  
XX  
PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for  
PS Identifying agents for treating tumours and autoimmune disease

Claim 1: Page 43-48; 85pp; French.

The present sequence encodes a human protein expressed in tumour cells.  
CC The polynucleotide is useful for screening cDNA/genomic DNA banks and  
CC for cloning isolated DNA: identifying mutant forms of the gene that  
CC encodes a human protein, where the mutations are associated with  
CC particular gene expression, or promoters and regulators of the gene,  
CC particularly for diagnosis, or promoters and regulators of the gene,  
CC as antisense probes and primers for recombinant expression of the gene,  
CC raising specific antibodies. The tumour expressed protein is useful for  
CC activity, bind to it or interact with it. These agents are potentially  
CC useful for treatment or prevention of disease. These agents are useful for  
CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic  
XX infections.

Sequence 3331 BP: 822 A; 945 C; 813 G; 751 T; 0 other:  
Query Match  
Best Local Similarity 97.78; Score 3258.8; DB 22; Length 3311;  
Matches 3277; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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QY 46 CAGGACAGGCTATGCTGAGCCCTGGGACAGCCACATCTCCGACAGCTCAGGGGA 105
DB 33 CCGGAGAGGTCTATGGCTGAGCCCTGGGACAGCCACATCTCTCCGACAGCTCAGGGGA 92
QY 106 AGAAGTGAAGAGGCGCATACCCCGGCTGTGGGCGCTGCTGCTGGGCGGAGCCGCTTC 165
DB 93 AGAAGTGAAGAGGCGCATACCCCGGCTGTGGGCGCTGCTGCTGGGCGGAGCCGCTTC 152
QY 166 CAGGTGACCCAGGAGGAGGAGCGAGCTTCAAGCCCTTCAAGAGCTGTAGTACCATAT 225
DB 153 CAGGTGACCCAGGAGGAGGAGCGAGCTTCAAGCCCTTCAAGAGCTGTAGTACCATAT 212
QY 226 GAGTACAGGCGGTGTGACAGCAGCGGTTCCAGGTGGAGGCTGGCGGCGCATACCCG 285
DB 213 GAGTACAGGCGGTGTGACAGCAGCGGTTCCAGGTGGAGGCTGGCGGCGCATACCCG 272
QY 286 GGCCTGTGACAGCAGCCTGCTGACCCCGTCAAGGCGACCGAGTCTCTTCTCTGCGAC 345
DB 273 GGCCTGTGACAGCAGCCTGCTGACCCCGTCAAGGCGACCGAGTCTCTTCTCTGCGAC 332
QY 346 GCGGGGAGTTCGTGATATGAGAGCAGCATGTAAAGCAATGGCTGAGGCGCGCTAC 405
DB 333 GCGGGGAGTTCGTGATATGAGAGCAGCATGTAAAGCAATGGCTGAGGCGCGCTAC 392
QY 406 TCCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 465
DB 393 TCCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 452
QY 466 CTCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 525
DB 453 CTCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 512
QY 526 TCCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 585
DB 513 TCCTCGGACAGCAGCCTGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 572
QY 586 CTGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 645
DB 573 CTGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 632
QY 646 GAGTCCAGCATCATCTTTGAGTTTTCGTTGAGATGAGCAGCAGTCCGACCCCAATGCAAT 705
DB 633 GAGTCCAGCATCATCTTTGAGTTTTCGTTGAGATGAGCAGCAGTCCGACCCCAATGCAAT 692
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us-10-046-433-39.rng

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QY 706 GAGTCCAGCATCATCTTTGAGTTTTCGTTGAGATGAGCAGCAGTCCGACCCCAATGCAAT 765
DB 693 GAGTCCAGCATCATCTTTGAGTTTTCGTTGAGATGAGCAGCAGTCCGACCCCAATGCAAT 752
QY 766 CGAGGCAATATATGCTCTCTATTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 752
DB 753 CGAGGCAATATATGCTCTCTATTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 812
QY 826 AACCTGCTGCTGAGAGAAACATTTCCATACAGGCTGCTCTCTCTCTCTCTCTCTCTCT 885
DB 813 AACCTGCTGCTGAGAGAAACATTTCCATACAGGCTGCTCTCTCTCTCTCTCTCTCTCT 872
QY 886 CCGTGGCAACCTGAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 945
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QY 946 GCCAATCTTATTAATTAAGAGAACTTCTGACACAGTGTGAGCAGCAGCAGCAGCAGCAG 1005
DB 933 GCCAATCTTATTAATTAAGAGAACTTCTGACACAGTGTGAGCAGCAGCAGCAGCAGCAG 992
QY 1006 TCAGAGAAAGATCTTCTCTCTGTAACGTGCGCCAGCTTGCACAGCAGCAGCAGCAGCAG 1052
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DB 1113 CCGAAATCTGTAAGCAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1172
QY 1186 ACCCACTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1245
DB 1173 ACCCACTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1232
QY 1246 TGCCCATATGCTTCTCTCTGTAACGTGCGCCAGCTTGCACAGCAGCAGCAGCAGCAG 1305
DB 1233 TGCCCATATGCTTCTCTCTGTAACGTGCGCCAGCTTGCACAGCAGCAGCAGCAGCAG 1292
QY 1306 CCGTGGCAACCTGAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1365
DB 1293 CCGTGGCAACCTGAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1352
QY 1366 GTTCTGAGTGGATCAACTGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1412
DB 1353 GTTCTGAGTGGATCAACTGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1405
QY 1426 CACATTTACAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1485
DB 1413 CACATTTACAGCAGCAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1472
QY 1486 CAGAGATTTAGACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1545
DB 1473 CAGAGATTTAGACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1532
QY 1546 ATGACATTTGCTTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1605
DB 1533 ATGACATTTGCTTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1592
QY 1606 GTGAATTTAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1665
DB 1593 GTGAATTTAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1652
QY 1666 TATACCTATCATATGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1725
DB 1653 TATACCTATCATATGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1712
QY 1726 ACTTTTCATGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1785
DB 1713 ACTTTTCATGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1772
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CC The polynucleotide is useful for screening cDNA/genomic DNA banks and  
 CC for cloning isolated DNA. Identifying mutant forms of the gene that  
 CC encodes a human protein, where the mutations are associated with  
 CC abnormal gene expression, or promoters and regulators of the gene that  
 CC protein; for diagnosis; for recombinant expression of the gene,  
 CC as antisense therapeutics. The tumour expressed and amplification,  
 CC activity, bind to it or interact with it. These agents are potentially  
 CC useful for treatment or prevention of diseases associated with abnormal  
 CC expression/activity of the protein, particularly immunological diseases  
 CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic  
 CC infections.

Sequence 2733 BP, 656 A; 783 C; 687 G; 607 T; 0 other;

Query Match 81.8%; Score 2726.6; DB 22; Length 2733;

Matches 2729; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 58 ATGGCTGAGCTGGGCAAGCCACCATCTCCCGCAGATCAAGGGAAGACTGAGAG 117  
 DB 1 ATGGCTGAGCTGGGCAAGCCACCATCTCCCGCAGATCAAGGGAAGACTGAGAG 117  
 QY 118 CGATTACCCCGCTGTGGGCGTGTCTCTGGGCTGGGAGCCGCTTCCAGGTACCCAG 60  
 DB 61 CGATTACCCCGCTGTGGGCGTGTCTCTGGGCTGGGAGCCGCTTCCAGGTACCCAG 60  
 QY 178 GGAAGGGAACGAGACTTCAAGCTTCAAGAGATCTGATACCACTATGATACAGGCG 120  
 DB 121 GGAAGGGAACGAGACTTCAAGCTTCAAGAGATCTGATACCACTATGATACAGGCG 120  
 QY 238 TGTGACAGACAGGGTTTCAGGTGAGGGTCCGCGCGGATACCCCGGCGCTGTGACCC 297  
 DB 181 TGTGACAGACAGGGTTTCAGGTGAGGGTCCGCGCGGATACCCCGGCGCTGTGACCC 297  
 QY 298 AGCTGCTGACCCCGCTGTGAGGGAACGAGATCTCTTCTCTGCAAGCCGCGGAGTTT 357  
 DB 241 AGCTGCTGACCCCGCTGTGAGGGAACGAGATCTCTTCTCTGCAAGCCGCGGAGTTT 357  
 QY 358 CTGGATATGAAGACCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 DB 301 CTGGATATGAAGACCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 418 GGCATTGCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417  
 DB 361 GGCATTGCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417  
 QY 478 ATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 DB 421 ATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 538 CCGCGGGGAGACTACATGCTTCAACAGGAGATGATGATGATGATGATGATGATGATGAT 537  
 DB 481 CCGCGGGGAGACTACATGCTTCAACAGGAGATGATGATGATGATGATGATGATGATGAT 480  
 QY 598 GTCAACTGAAGCAATCTGACCGCTTCAACAGGAGATGATGATGATGATGATGATGAT 540  
 DB 541 GTCAACTGAAGCAATCTGACCGCTTCAACAGGAGATGATGATGATGATGATGATGAT 540  
 QY 658 ATCTTTAGTTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 DB 601 ATCTTTAGTTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 QY 718 ATGAAGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 DB 661 ATGAAGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
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 QY 838 GTGAGAAACATTCGCAATACAGGGGTGCTACACTTCAAGATGCTTCCCTGCAAACT 897

DB 701 GTGAGAAACATTCGCAATACAGGGGTGCTACACTTCAAGATGCTTCCCTGCAAACT 897  
 QY 898 GGCAGCTATGCAAGACAGAGGCTCCCTTTTGTGCAAACTTTGCGGCAACTCTTAT 840  
 DB 841 GGCAGCTATGCAAGACAGAGGCTCCCTTTTGTGCAAACTTTGCGGCAACTCTTAT 840  
 QY 958 TCAATTAAGAGAACTTCTTTCAGACAGTGTGACCTGTCAATATCTAGAGAAAGA 1017  
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 QY 1018 TCTTCTTCTGTAACGTTGGGCGCCAGCTGTGACAGACAAAGATTTATTTTACACACAG 960  
 DB 961 TCTTCTTCTGTAACGTTGGGCGCCAGCTGTGACAGACAAAGATTTATTTTACACACAG 960  
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 QY 1138 AGCAGAGACTTGTAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 DB 1081 AGCAGAGACTTGTAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
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 QY 1378 ATCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
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 QY 1438 GCTGCTGAGACCTTCAACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1437  
 DB 1381 GCTGCTGAGACCTTCAACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 QY 1498 CCTTCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 DB 1441 CCTTCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 QY 1558 TTTGAGACCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 DB 1501 TTTGAGACCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 QY 1618 ACCAACACTCTTGTGAG 1560  
 DB 1561 ACCAACACTCTTGTGAG 1560  
 QY 1678 ATTGAGAGAAACATTCGCAATACAGGGGTGCTACACTTCAAGATGCTTCCCTGCAAACT 1620  
 DB 1621 ATTGAGAGAAACATTCGCAATACAGGGGTGCTACACTTCAAGATGCTTCCCTGCAAACT 1620  
 QY 1738 GCAAGCAGAGATGACAGCTTCAACAGGAGATGATGATGATGATGATGATGATGATGAT 1737  
 DB 1681 GCAAGCAGAGATGACAGCTTCAACAGGAGATGATGATGATGATGATGATGATGATGAT 1680  
 QY 1798 ATGAATGAGCTGTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
 DB 1741 ATGAATGAGCTGTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
 QY 1858 TCTTGCACCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 DB 1801 TCTTGCACCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 QY 1918 TGCCCGCTTACCAATTTGAAAGCCACAGCTTATGAGTGTGACAGGCTGTGCGCC 1977

XX	Key	Location/Qualifiers
FH	CDS	1..2610
FT		/tag= a
FT		/product= "tumour expressed protein"
XX		
PN		WO2001J31003-A1.
PD		03-MAY-2001.
XX		
XX		30-OCT-2000; 2000OWO-FR03032.
PF		
XX		
PR		29-OCT-1999; 99FR-0013629.
XX		
PA		(FABR ) FABRE MEDICAMENT SA PIERRE.
XX		
PI		Deleste Y, Magistrelli G, Jeanin P, Bonnefoy J;
DR		WPI: 2001-328651/34.
DR		P-PADB; AAB83851.
XX		New nucleic acid, expressed in tumours and lymphoid tissue is useful for
FT		identifying agents for treating tumours and autoimmune disease -
XX		
PS		Claim 2: Page 63-67; 85pp; French.
XX		The present sequence encodes a human protein expressed in tumor cells.
CC		The polynucleotide is useful for screening cDNA/genomic DNA banks and
CC		for cloning isolated DNA; identifying mutant forms of the gene that
CC		encodes a human protein, where the mutations are associated with
CC		abnormal gene expression, or promoters and regulators of the gene,
CC		particularly for diagnosis, for recombinant expression and amplification; and
CC		protein; as probes and primers for detection and amplification; and
CC		as antisense therapeutics. The tumor expressed protein is useful for
CC		raising specific antibodies and to screen agents that modulate its
CC		activity, bind to it or interact with it. These agents are potentially
CC		useful for treatment or prevention of diseases associated with abnormal
CC		expression/activity of the protein, particularly immunological diseases
CC		(autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
CC		Infections.
SO		Sequence 2610 BP; 634 A; 744 C; 644 G; 588 T; 0 other;
QY	Query Match	78.1%; Score 2603.6; DB 22; Length 2610;
	Best Local Similarity	99.8%; Pred. No. 0;
	Matches 2606; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	181	ACGGGACCAGGACTTCACGCCCTCGCAAAAGACTGTGAATGCACATGATGATACACGGCGTGT 240
DB	1	ACGGGACCAGGACTTCATGCTCGAAGAAGTCTGATACCATATGATATACACGGCGTGT 60
OY	241	GACAGCAGCGGTTCCAGGTGAGAGGGTGCCCTGCCCATACCCGGGGCGTGTGCACACAGC 300
DB	61	GAGAGCACGGGTTCCAGGTGAGAGGGTGCCCGTCCGCATACCCGGGGCGTGTGCACACAGC 120
OY	301	CTGCCTGACCCCGCTTAAGGACACGAGAGTCTCTTCTCTGCAAGCGGGGAGTTTGTG 360
DB	121	CTGCCTGACCCCGCTTAAGGACACGAGAGTCTCTTCTCTGCAAGCGGGGAGTTTGTG 180
OY	361	GATTGTAAGGACCACTCATGTAAAGCCATAGCGGCTGTGGGCGGCTACTCCCTGGACAGGC 420
DB	181	GATTGTAAGGACCACTCATGTAAAGCCATAGCGGCTGTGGGCGGCTACTCCCTGGACAGGC 240
OY	421	ATTGGGTTTATGATGTGTGATGAGTACGTGCCCATGTGCTTTGGACACCTCTTAGCCAACATG 480
DB	241	ATTGGGTTTATGATGTGTGATGAGTACGTGCCCATGTGCTTTGGACACCTCTTAGCCAACATG 300
OY	481	GAGCTGATGATACAGTGTCTGCTGATGCTACACGGGAACTGACTTCTGTCTCCAAATGGGTTCCC 540
DB	301	GAGCTGATGATACAGTGTCTGCTGATGCTACACGGGAACTGACTTCTGTCTCCAAATGGGTTCCC 360
OY	541	CGGGGGAGATATACGCTTACACGGGAGATGACAGCCACACTGATGTAGCGGTC 600

D	361	CGGGGGGACTACATGCGCCCTCCCAACGAGGAGATGCACGACCCACTGATGTACCGCGTC	420
O	601	AACCTTAAGCAATCTGGCACCCTTACCTTGAATTACTACTATCCAGACCCAGCATCATC	660
D	421	AACCTGAAGCAATCTGGCACCCTTAACTTAACTACTATCCAGACCCAGCATCATC	480
O	661	TTTGAGTTTTCGTTCCGAATGACCACTGCGACCCCAAGCAGATGACTCCAGGTGATG	720
D	481	TTTGAGTTTTCGTTCCGAATGACCACTGCGACCCCAAGCAGATGACTCCAGGTGATG	540
O	721	AAGACCCAGAGAAAGGATGGAAATTCACACTGTGTGGAGCTTAATCGAGCAATTAATGTC	780
D	541	AAGACCCAGAGAAAGGATGGAAATTCACACTGTGTGGAGCTTAATCGAGCAATTAATGTC	840
O	781	CTTATTGGAGAACCCACAGCTTCTTCAGTATGACCAAAAGTACCAAGCTGTGTGGAG	600
D	601	CTTATTGGAGAACCCACAGCTTCTTCAGTATGACCAAAAGTACCAAGCTGTGTGGAG	660
O	841	AGAAACATTGGCAATTAACAGGGGTGGCTTACACTTCAAAATGCTTCCCGTCAAACTCTG	900
D	661	AGAAACATTGGCAATTAACAGGGGTGGCTTACACTTCAAAATGCTTCCCGTCAAACTCTG	720
O	901	ACCTATGACAGACAGCAAGGGGCTCTCTTCTGCAACTTTTCCAGCCAGCTTATTAACA	960
D	721	ACCTATGACAGACAGCAAGGGGCTCTCTTCTGCAACTTTTCCAGCCAGCTTATTAACA	780
O	961	AATAAGAGAGAACTCTTCTGCAACTGTGACAGCTTCAAAATGCTTCCCGTCAAACTCTG	1020
D	781	AATAAGAGAGAACTCTTCTGCAACTGTGACAGCTTCAAAATGCTTCCCGTCAAACTCTG	840
O	1021	TCTTCTGTAGAGTGGGCCCCAGCTTTCACAGACAAAGATTTATTTCTACACACACAGGCT	1080
D	841	TCTTCTGTAGAGTGGGCCCCAGCTTTCACAGACAAAGATTTATTTCTACACACACAGGCT	900
O	1081	TGGGATGCAACGAGAGACACAACTAGTACAAATAGGGCCCAAGCCGAAATCTGTAGC	1140
D	901	TGGGATGCAACGAGAGACACAACTAGTACAAATAGGGCCCAAGCCGAAATCTGTAGC	960
O	1141	GAGGACCTTGAGGGGCAAGTGAAGCTGCTGTGTGTGAAGCCACAGCCGACCCACC	1200
D	961	GAGGACCTTGAGGGGCAAGTGAAGCTGCTGTGTGTGAAGCCACAGCCGACCCACC	1020
O	1201	TGCACCCAGGCTTCTTCAAAACCAACACAGCACTGCGACCCCTGGCCATATGTTCTC	1260
D	1021	TGCACCCAGGCTTCTTCAAAACCAACACAGCACTGCGACCCCTGGCCATATGTTCTC	1080
O	1261	TACTCCTAATGCTGAGACTGTACCGCTGCTCCGCGAGGAGCTGAACCTGCTGTGGATTT	1320
D	1081	TACTCCTAATGCTGAGACTGTACCGCTGCTCCGCGAGGAGCTGAACCTGCTGTGGATTT	1140
O	1321	GAATACAAATGCTGAGAAACGCTGCCCAAAACATGGAAGACGCGTTCAGATGGGATC	1380
D	1141	GAATACAAATGCTGAGAAACGCTGCCCAAAACATGGAAGACGCGTTCAGATGGGATC	1200
O	1381	AACCTGAGTACAGAGGCAATGATCATGATTTCTCACTCTGTTGTGCGAGATTTAGACCT	1440
D	1201	AACCTGAGTACAGAGGCAATGATCATGATTTCTCACTCTGTTGTGCGAGATTTAGACCT	1260
O	1441	GCTGAGGCTGAGCAATGATCATGATTTCTCACTCTGTTGTGCGAGATTTAGACCT	1500
D	1261	GCTGAGGCTGAGCAATGATCATGATTTCTCACTCTGTTGTGCGAGATTTAGACCT	1320
O	1501	CCGAGCTGGGATGAGCAACAGAAATTAAGAGGTGGCCAGAAATCAATTTGCTTTT	1560
D	1321	CCGAGCTGGGATGAGCAACAGAAATTAAGAGGTGGCCAGAAATCAATTTGCTTTT	1380
O	1561	GAGACCCCTTCTGTGAACTGTGACTCTTCACTTCAATGGTGGTGTGAATTTAGAGCC	1620
D	1381	GAGACCCCTTCTGTGAACTGTGACTCTTCACTTCAATGGTGGTGTGAATTTAGAGCC	1440
O	1621	AACCTCTCTGTGAGACGTTGAAAGGTTTCCAAAGGCAACAGTCTTATACCTTCAATCAT	1680
D	1441	AACCTCTCTGTGAGACGTTGAAAGGTTTCCAAAGGCAACAGTCTTATACCTTCAATCAT	1500
O	1681	GAGGAGAACCTTCCACAGGCTTACCTGAGGCTTCCAGAGACCACTTTTATGAGCA	1740
D	1501	GAGGAGAACCTTCCACAGGCTTACCTGAGGCTTCCAGAGACCACTTTTATGAGCA	1560
O	1741	AGCAGAGATACCAACATGAGCTTGGCAAGATTTACTCTCAATGATACCAATTTATG	1800
D	1561	AGCAGAGATACCAACATGAGCTTGGCAAGATTTACTCTCAATGATACCAATTTATG	1620
O	1801	AATGGGCTGGCTCTACTGTGCTGCTTACTATTTGACCGAGATTTAGAGACCTGCACTCTG	1860
D	1621	AATGGGCTGGCTCTACTGTGCTGCTTACTATTTGACCGAGATTTAGAGACCTGCACTCTG	1680
O	1861	ATGAGCTGTGCTCTCTGCTGCTTACTATTTGACCGAGATTTAGAGACCTGCACTCTG	1920
D	1681	ATGAGCTGTGCTCTCTGCTGCTTACTATTTGACCGAGATTTAGAGACCTGCACTCTG	1740
O	1921	CCGCTTAACAAATTTGAAAGCCCAACAGCTTATGCTGTGACAGGCTGTGGGCTCTG	1980
D	1741	CCGCTTAACAAATTTGAAAGCCCAACAGCTTATGCTGTGACAGGCTGTGGGCTCTG	1800
O	1981	GCTCAGGAGCAACAGAACACAAAGATTCACCTCTGTGCTACAAATTTGACCTTTTCA	2040
D	1801	GCTCAGGAGCAACAGAACACAAAGATTCACCTCTGTGCTACAAATTTGACCTTTTCA	1860
O	2041	CGCAGACTTCCACAGGAGCTTTCACCTTCACTTCCGCTTTGGCAACACGCTCACT	2100
D	1861	CGCAGACTTCCACAGGAGCTTTCACCTTCACTTCCGCTTTGGCAACACGCTCACT	1920
O	2101	CTTGTGAGAGGCCAGGCTTCTTCAAAAGGTTGAAATCTTCCATCACTTTACCTTC	2160
D	1921	CTTGTGAGAGGCCAGGCTTCTTCAAAAGGTTGAAATCTTCCATCACTTTACCTTC	1980
O	2161	AGTCTGTGTGAAACCAAGGATGAGAAATGCTGTGTGACCCGCAATTTGACCTTC	2220
D	1981	AGTCTGTGTGAAACCAAGGATGAGAAATGCTGTGTGACCCGCAATTTGACCTTC	2040
O	2221	CGGATTCCTGAGGCTGAGTCAAGGTTTCCAAATTTACACGCTTACGCTTCCAGGCA	2280
D	2041	CGGATTCCTGAGGCTGAGTCAAGGTTTCCAAATTTACACGCTTACGCTTCCAGGCA	2100
O	2281	GTCATCATCCCCCAGAGGCTGACAGCTTCAAGGCTGGGGTTTCTCACAGCTTCTACG	2340
D	2101	GTCATCATCCCCCAGAGGCTGACAGCTTCAAGGCTGGGGTTTCTCACAGCTTCTACG	2220
O	2341	CTTGTGATGACCTTATTTGGGCTGACAAAGATATGATCTGTGATGATCACTTCCCA	2400
D	2161	CTTGTGATGACCTTATTTGGGCTGACAAAGATATGATCTGTGATGATCACTTCCCA	2280
O	2401	GCTGAACCTTTCACCTGAGATCTGTTGGGAAATACCGGAGTGTATCTTTTATAGTGC	2460
D	2221	GCTGAACCTTTCACCTGAGATCTGTTGGGAAATACCGGAGTGTATCTTTTATAGTGC	2340
O	2461	AATGATGTGACCCAGCTCTGCAATTTTGGAGATCAACACATCTCCGCTCAGGTCACT	2520
D	2281	AATGATGTGACCCAGCTCTGCAATTTTGGAGATCAACACATCTCCGCTCAGGTCACT	2400
O	2521	CCAC	

QY 2761 TGCAGAACATAGATTTCTGCTGAAGTG 2790  
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Db 2581 TGCAGAACATAGATTTCTGCTGAAGTG 2610

RESULT 7  
AAF27997  
ID AAF27997 standard; DNA: 2554 BP.

AC AAF27997;

DT 08-MAY-2001 (first entry)

DE Human TR13 receptor coding sequence SEQ ID NO: 1.

KW Human: tumour necrosis factor receptor; TR13; TR14; infection;

KW cancer; autoimmune disease; allergy; inflammatory disease;

KW graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.

OS Homo sapiens.

PN WO200105834-A1.

PD 25-JAN-2001.

PF 14-JUL-2000; 2000WO-US19343.

PR 16-JUL-1999; 99US-0144087.

PR 18-AUG-1999; 99US-0149450.

PR 20-AUG-1999; 99US-0149712.

PR 10-SEP-1999; 99US-0153089.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Ni J, Young PE;

DR WPI: 2001-112682/12.

DR F-PSDB; AAB35328.

PT Nucleic acids encoding 2 human tumor necrosis factor receptor

PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis

PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and

PT hypohidrotic ectodermal dysplasia -

PS Claim 2; Page 366-369; 418pp; English.

CC The present invention provides the protein and coding sequences of the

CC human tumour necrosis factor receptors TR13 and TR14. These sequences are

CC useful in the diagnosis and treatment of many diseases, including cancer,

CC autoimmune diseases, cardiovascular disorders, allergies,

CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and

CC infections.

XX Sequence 2554 BP; 642 A; 722 C; 588 G; 602 T; 0 other;

XX

Query Match 75.8%; Score 2527.4; DB 22; Length 2554;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2539; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 794 CCACAGCTTCTCATGATGAGCAACCAAGTACCCAGCTGTGCTGAGAAACATTGCCA 853

Db 15 CCGGAGCTTCTCATGATGAGCAACCAAGTACCCAGCTGTGCTGAGAAACATTGCCA 74

QY 854 TAAACAGGGTGGCTTACACTTCAAGATGCTCCCTGCAAACTGACAGTATGACAGA 913

Db 75 TAAACAGGGTGGCTTACACTTCAAGATGCTCCCTGCAAACTGACAGTATGACAGA 134

QY 914 AGCAGGCTCTCTTCTGCAAACTTGCACCAACTCTTATCAAAATAAGAGGAAA 973

Db 135 AGCAGGCTCTCTTCTGCAAACTTGCACCAACTCTTATCAAAATAAGAGGAAA 193

QY 974 CTCTTGCACACAGTGTGACCTGACAAATACAGAGAAAGATCTTCTCTGTAAG 1033

Db 194 CTCTTGCACACAGTGTGACCTGACAAATACAGAGAAAGATCTTCTCTGTAAG 253

QY 1034 TCGGCCCACTTGCACAGCAACAAAGATTATTCTACACACACAGGCTGCGATGCCAACG 1093

Db 254 TCGGCCCACTTGCACAGCAACAAAGATTATTCTACACACACAGGCTGCGATGCCAACG 313

QY 1094 GAGAGACACACTCATGTATCAAAATGGGCGCAACCGGAAATCTGTAGCGNAGACCTTGAGG 1153

Db 314 GAGAGACACACTCATGTATCAAAATGGGCGCAACCGGAAATCTGTAGCGNAGACCTTGAGG 373

QY 1154 GGGCAGTGAAGCTGCTGCTCTGTGTGAAGACCACTGCCCCACCTGCCAACCCAGGCT 1213

Db 374 GGGCAGTGAAGCTGCTGCTCTGTGTGAAGACCACTGCCCCACCTGCCAACCCAGGCT 433

QY 1214 TCTTCAAAACCAACACAGACCTGCGACCCGCGCCATATGATGTTCTACTCCAAATGGCT 1273

Db 434 TCTTCAAAACCAACACAGACCTGCGACCCGCGCCATATGATGTTCTACTCCAAATGGCT 493

QY 1274 CAGACTGTACCCGCTGCGCTGCGAGGAGCTGAACCTGCTGGGATTTGAATACAAATGGT 1333

Db 494 CAGACTGTACCCGCTGCGCTGCGAGGAGCTGAACCTGCTGGGATTTGAATACAAATGGT 553

QY 1334 GGAACACGCTGCCCAACAAACATGGAACGACCGCTTCTCAAGTGAATCACTTGAATGCT 1393

Db 554 GGAACACGCTGCCCAACAAACATGGAACGACCGCTTCTCAAGTGAATCACTTGAATGCT 613

QY 1394 AGGCGATGACAGGCTGGAGGTGGCTGTGATGATACATTTACACAGCTGTGAGACCTCAG 1453

Db 614 AGGCGATGACAGGCTGGAGGTGGCTGTGATGATACATTTACACAGCTGTGAGACCTCAG 673

QY 1454 ACAATGACTTCATGATTTCTACCTGTGTTGCGAGATTTAACTCCGCACTCGGTGA 1513

Db 674 ACAATGACTTCATGATTTCTACCTGTGTTGCGAGATTTAACTCCGCACTCGGTGA 733

QY 1514 TGGCAGACACAGAAATTAAGAGGTGGCGAATACATTTGCTTGAAGACCTCTGTG 1573

Db 734 TGGCAGACACAGAAATTAAGAGGTGGCGAATACATTTGCTTGAAGACCTCTGTG 793

QY 1574 CTGTGAACCTGAGCTCTTACTTCAATGTGTGGGTGTAATCTTAGACCAACACTCTGTG 1633

Db 794 CTGTGAACCTGAGCTCTTACTTCAATGTGTGGGTGTAATCTTAGACCAACACTCTGTG 853

QY 1634 AGAGCTGGAAGTTTCCAAAGGCAACAGCTTACTTCAATGATGAGAGAACTGA 1693

Db 854 AGAGCTGGAAGTTTCCAAAGGCAACAGCTTACTTCAATGATGAGAGAACTGA 913

QY 1694 CCACGAGCTTACCTGGGCTTCCAGAGGACCACTTTCATGAGCAAGCAAGATGACA 1753

Db 914 CCACGAGCTTACCTGGGCTTCCAGAGGACCACTTTCATGAGCAAGCAAGATGACA 973

QY 1754 CCAATGACGTTGCCAAGATCTACTCATCAATGTCACCAATGTTATGATGAGGCTGCT 1813

Db 974 CCAATGACGTTGCCAAGATCTACTCATCAATGTCACCAATGTTATGATGAGGCTGCT 1033

QY 1814 CCTACTGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1873

Db 1034 CCTACTGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1093

QY 1874 CTGCTGCTTACTATATTTAGACGAGATTCAGGAACCTGCACTCTGCCCCCTTAACAAA 1933

Db 1094 CTGCTGCTTACTATATTTAGACGAGATTCAGGAACCTGCACTCTGCCCCCTTAACAAA 1153

QY 1934 TTCTGAAAGCCCAACAGCTTATGCTGTGTCAGAGCTGTGCTGCTGCTGCTGCTGCT 1993

Db 1154 TTCTGAAAGCCCAACAGCTTATGCTGTGTCAGAGCTGTGCTGCTGCTGCTGCTGCT 1213

QY 1994 AGAACAACAGATTCAGCTGTGCTCAATGATTTGACCTTCTCAAGCAACTCCAA 2053

Db 1214 AGAACAACAGATTCAGCTGTGCTCAATGATTTGACCTTCTCAAGCAACTCCAA 1273

QY 2054 CCAGGACTTTCACATCAACATTTCTCCGCTTGGCAACACCGTCACTTTGCTGAGAGGC 2113

Db 1274 CCAGGACTTTCACATCAACATTTCTCCGCTTGGCAACACCGTCACTTTGCTGAGAGGC 1333

QY 2114 CAAGCTTCACTTCCAAAGGTTGAATATCTTCATCTCACTTTACCTTCAGTCTCTGTGAA 2173  
 DB 1334 CAAGCTTCACTTCCAAAGGTTGAATATCTTCATCTCACTTTACCTTCAGTCTCTGTGAA 1393  
 QY 2174 ACCAGGTTAGAAATATGCTGTGTGACCGCAATATGTCACCTGACCTCCGATTCCTGAG 2233  
 DB 1394 ACCAGGTTAGAAATATGCTGTGTGACCGCAATATGTCACCTGACCTCCGATTCCTGAG 1453  
 QY 2234 GTGACTCAGGGTTCCTCCAAATCTATCAAGCTACGCTGCGCAGGAGTCAATCTCCCC 2293  
 DB 1454 GTGACTCAGGGTTCCTCCAAATCTATCAAGCTACGCTGCGCAGGAGTCAATCTCCCC 1513  
 QY 2294 CAGAGGTGACAGGCTACAAAGCCGGGGTTTCTCAGACGCTGACGCTTGCTGATGAC 2353  
 DB 1514 CAGAGGTGACAGGCTACAAAGCCGGGGTTTCTCAGACGCTGACGCTTGCTGATGAC 1573  
 QY 2354 TTATTTGGGGTACAAACAGATATGACTGTGATGGAATCACCCTCCAGCTGAATCTTTCC 2413  
 DB 1574 TTATTTGGGGTACAAACAGATATGACTGTGATGGAATCACCCTCCAGCTGAATCTTTCC 1633  
 QY 2414 ACCTGAGTCTCTGGGAATACCGAGCTGATCTTTTATAGGTCCAAATGATGACCC 2473  
 DB 1634 ACCTGAGTCTCTGGGAATACCGAGCTGATCTTTTATAGGTCCAAATGATGACCC 1693  
 QY 2474 AGTCTGCACTTCTGGAGATCAACACCATCCGCTCAGGTGACAGTCCAGAAAACTG 2533  
 DB 1694 AGTCTGCACTTCTGGAGATCAACACCATCCGCTCAGGTGACAGTCCAGAAAACTG 1753  
 QY 2534 TCCCTGGAAGTTGCTCTCCAGGAAGCTGATGAGTGGGACTGTGATGGCTGCAACT 2593  
 DB 1754 TCCCTGGAAGTTGCTCTCCAGGAAGCTGATGAGTGGGACTGTGATGGCTGCAACT 1813  
 QY 2594 TCCACTTCTGTGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2653  
 DB 1814 TCCACTTCTGTGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1873  
 QY 2654 CTATGCTCAGCAGCTGTGTGGCTGGATCCAGAAAGTACTTACGTGTGGCGGAACCA 2713  
 DB 1874 CTATGCTCAGCAGCTGTGTGGCTGGATCCAGAAAGTACTTACGTGTGGCGGAACCA 1933  
 QY 2714 AGCTATGCTGTGTGGCTGTCTGCTGCTGAGAGAGTACCATCTGCAAAACCATATG 2773  
 DB 1934 AGCTATGCTGTGTGGCTGTCTGCTGCTGAGAGAGTACCATCTGCAAAACCATATG 1993  
 QY 2774 ATTTCTGCTGGAAGTGGCATCTGCAAGCACTGTACTGCTGCTGCTGCTGCTGCT 2833  
 DB 1994 ATTTCTGCTGGAAGTGGCATCTGCAAGCACTGTACTGCTGCTGCTGCTGCTGCTGCT 2053  
 QY 2834 TGACCTGCTACTTTTGGAAAAAATCAAAACTAGATNCAAGTACTTCAAGCTGTGTA 2893  
 DB 2054 TGACCTGCTACTTTTGGAAAAAATCAAAACTAGATNCAAGTACTTCAAGCTGTGTA 2113  
 QY 2894 TGAATGCTACTTCAAGAGCTGTGACCTGCGCAGAGTACAGCTGCGCATCATGGAAG 2953  
 DB 2114 TGAATGCTACTTCAAGAGCTGTGACCTGCGCAGAGTACAGCTGCGCATCATGGAAG 2173  
 QY 2954 GCGAGATTAAGAGAGCACTCATCTTTACAGCAAGATCATCTTTGGGAGATCAA 3013  
 DB 2174 GCGAGATTAAGAGAGCACTCATCTTTACAGCAAGATCATCTTTGGGAGATCAA 2233  
 QY 3014 ATCATTTACTTCAAGAGAGCTGATGATGATTTGATGATGATGATGATGATGATGATG 3073  
 DB 2234 ATCATTTACTTCAAGAGAGCTGATGATGATTTGATGATGATGATGATGATGATGATG 2293  
 QY 3074 AGAGGCGCCAGACATGACCTGTGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 3133  
 DB 2294 AGAGGCGCCAGACATGACCTGTGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2353  
 QY 3134 CATAGACCTTTGCAAGGCTGCGGGATTTGGGTGCGCAGCATCTGCGCAACCCACTGCT 3193  
 DB 2354 CATAGACCTTTGCAAGGCTGCGGGATTTGGGTGCGCAGCATCTGCGCAACCCACTGCT 2413

QY 3194 GGAATATCTTTCATTTGGCTTATATGATGTTGAATTTGAGATCTTTTATAGACT 3253  
 DB 2414 GGAATATCTTTCATTTGGCTTATATGATGTTGAATTTGAGATCTTTTATAGACT 2473  
 QY 3254 ACCAAACCTCTTCTGCTTGTGCTCAAAACCTGCCAAATATACCACTGTTTGA 3313  
 DB 2474 ACCAAACCTCTTCTGCTTGTGCTCAAAACCTGCCAAATATACCACTGTTTGA 2533  
 QY 3314 AATTTAAAAAATTTAAAAA 3334  
 DB 2534 AATTTAAAAAATTTAAAAA 2554

## RESULT 8

AAZ41991  
ID AAZ41991 standard; cDNA; 1717 BP.

AAZ41991;

31-JAN-2000 (first entry)

DE Human endometrium tumour cDNA derived EST 11.

KW Endometrium; human; tumour; cancer; anticancer; cytostatic; EST; treatment; uterine; gene therapy; expressed sequence tag; ss.

OS Homo sapiens.

DE19817948-A1.

PD 21-OCT-1999.

PF 17-APR-1998; 98DE-1017948.

PR 17-APR-1998; 98DE-1017948.

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

ROSENTHAL A, SPECHT T, HINZMANN B, SCHMITT A, PILARSKY C, DAHL E;

WPI: 1999-591957/51.

DR P-PSDB; AAY59971, AAY59972, AAY59973.

PT New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents

PS Claim 3; Page 172; 444pp; German.

CC This invention describes novel human nucleic acid (cDNA) sequences (A),  
 CC that are highly expressed in uterine tumour tissue and which have  
 CC anticancer and cytostatic activity. (A) are used (i) for recombinant  
 CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)  
 CC are used (i) to identify agents suitable for treatment of uterine or  
 CC endometrial cancer; (ii) directly for treating these forms of cancer  
 CC (including expression from gene therapy vectors) and (iii) for  
 CC generation of specific antibodies. (A) are identified by assembling ESTs  
 CC (expressed sequence tags) from a particular tissue type before comparison  
 CC of expression patterns. This allows a significantly longer fragment of  
 CC the gene to be revealed, so should reduce the number of failures  
 CC associated with the fact that ESTs from different libraries may represent  
 CC different parts of the same unknown gene, distorting the estimated  
 CC frequency of occurrence in a particular tissue. AAZ41981-242121 represent  
 CC EST fragments derived from a human endometrium tumour cDNA library which  
 CC encode the protein sequences represented in AAY59941-160328.

SO Sequence 1717 BP; 416 A; 492 C; 388 G; 421 T; 0 other;

Query Match 51.1%; Score 1705; DB 20; Length 1717;

Best local similarity 99.9%; Pred. No. 0;

Matches 1716; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1610 ATTCTAGACCAACACTCTCTGTGGAGAGCTGGAAGTTCCAAAGGCAACAGTCTATTA 1669

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|||||
Db 1 ATTTAGAGCAGACACTCTGTGGAGCTGAAAGTTCCAAAGGCAAAAGTCCTATA 60
1670 CCTACATATGAGAGAGAACACTACACAGACTTCCACTGGGCTTCAGAGGACACTT 1729
|||||
Db 61 CCTACATATGAGAGAGAACACTACACAGACTTCCACTGGGCTTCAGAGGACACTT 120
1730 TTTCATGAGGCAAGAGAGATACACATGACGTTGCCAAGATCTACTCCATCATGTCA 1789
|||||
Db 121 TTTCATGAGGCAAGAGAGATACACATGACGTTGCCAAGATCTACTCCATCATGTCA 180
1790 CCAATGTTATGATGAGGCGGCTCTACTGCGCTGCTGAGGCTTACAGGCTGTGATG 1849
|||||
Db 181 CCAATGTTATGATGAGGCGGCTCTACTGCGCTGCTGAGGCTTACAGGCTGTGATG 240
1850 TGGGCTCTCTGCACTCTTGTCTGCTGCTGTTACTATATGACGAGATTCCAGAACCT 1909
|||||
Db 241 TGGGCTCTCTGCACTCTTGTCTGCTGCTGTTACTATATGACGAGATTCCAGAACCT 300
1910 GCCACTCTGCCCCCTTAACACAAATTTGAAAGCCACAGCTTATGCTGTCCAGGCT 1969
|||||
Db 301 GCCACTCTGCCCCCTTAACACAAATTTGAAAGCCACAGCTTATGCTGTCCAGGCT 360
1970 GGTGCTCCCTGTGTCAGGAGCAAGAACACAGATCCACTCTGTGCTCAATGATT 2029
|||||
Db 361 GTGTGCTCCCTGTGTCAGGAGCAAGAACACAGATCCACTCTGTGCTCAATGATT 420
2030 GCACCTTTCACAGCAACACTCCACAGAGCTTTCACACTCAACCTTCCGCTTTGGCAA 2089
|||||
Db 421 GCACCTTTCACAGCAACACTCCACAGAGCTTTCACACTCAACCTTCCGCTTTGGCAA 480
2090 ACACCTCTACTCTGTGTGAGGCGCAAGCTTCACTTCCAAAGGTTGAAATCTTCCATC 2149
|||||
Db 481 ACACCTCTACTCTGTGTGAGGCGCAAGCTTCACTTCCAAAGGTTGAAATCTTCCATC 540
2150 ACTTACCTCTCACTCTGTGTGAAACACAGAGTGGAAATGCTGTGTGACACGCAATG 2209
|||||
Db 541 ACTTACCTCTCACTCTGTGTGAAACACAGAGTGGAAATGCTGTGTGACACGCAATG 600
2210 TCACCTACCTCCGGATTTCTGAGGCTGAGTCAAGGCTTCCAAATCTATCACAGCTACG 2269
601 TCACCTACCTCCGGATTTCTGAGGCTGAGTCAAGGCTTCCAAATCTATCACAGCTACG 660
2270 TCTGCCAGGAGTCATCATCTCCCGAGAGTGAAGGCTACAGGCTGAGGCTTCTCTAC 2329
661 TCTGCCAGGAGTCATCATCTCCCGAGAGTGAAGGCTACAGGCTGAGGCTTCTCTAC 720
2330 AGCCTGTCAGACCTTGTGATGCACTATTGGGGTGACAACAGATATGACTGTGATGAA 2389
|||||
Db 721 AGCCTGTCAGACCTTGTGATGCACTATTGGGGTGACAACAGATATGACTGTGATGAA 780
2390 TCACCTCCCGAGTGAACCTTTTCCACCTGAGTCTTGGGAATACCGGACGTGATCTT 2449
781 TCACCTCCCGAGTGAACCTTTTCCACCTGAGTCTTGGGAATACCGGACGTGATCTT 840
2450 TTTATAGTCCATGATGATGAGACCAAGTCCGTCGACTCTGGGAGATCAACACATCCGG 2509
|||||
Db 841 TTTATAGTCCATGATGATGAGACCAAGTCCGTCGACTCTGGGAGATCAACACATCCGG 900
2510 TCAGTGCACTCCACAGAAAAGTCCCTGGAAGTTGCTGCTGCCAGAGAGCTGTCAG 2569
901 TCAGTGCACTCCACAGAAAAGTCCCTGGAAGTTGCTGCTGCCAGAGAGCTGTCAG 960
2570 ATGGGACCTGTGATGGCTGGAATCTCCACTCTCTGTGGAGAGAGCGGCTGTGCCGC 2629
961 ATGGGACCTGTGATGGCTGGAATCTCCACTCTCTGTGGAGAGAGCGGCTGTGCCGC 1020
2630 TCTGCTAGTGGCTGACTACATGCTATGCTACAGAGCTGTGTGGCTGGGATCCAGAGA 2689
1021 TCTGCTAGTGGCTGACTACATGCTATGCTACAGAGCTGTGTGGCTGGGATCCAGAGA 1080
2690 CTACTTACGTGTGGCGAAGCCAGGCTATGCTGTGGTGGCAATTTCTGTGCTGACAGA 2749
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Db 1081 CTACTTACGTGTGGCGAAGAACCCAGCTATGCTGTGGTGCATTTCTGCTGACAGAGA 1140
QY 2750 GAGTCACCATCTGCAAAACCATAGATTTCGTGGTGAAGTGGCATCTGTGAGGACCT 2809
Db 1141 GAGTCACCATCTGCAAAACCATAGATTTCGTGGTGAAGTGGCATCTGTGAGGACCT 1200
QY 2810 GTATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2869
Db 1201 GTATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 2870 AGTACAGTACTCCAGCTGCTGATGATCTCTCTCAAGAGCTGTGACTCTCCAGCAG 2929
Db 1261 AGTACAGTACTCCAGCTGCTGATGATCTCTCTCAAGAGCTGTGACTCTCCAGCAG 1320
QY 2930 CTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2989
Db 1321 CTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 2990 AGAA-TCACCTTTTGGGAGATCAAAATCAATTAACCTCCAAAGAGACTCTGATGATTG 3048
Db 1381 AGAAGTCACTCTTTGGGAGATCAAAATCAATTAACCTCCAAAGAGACTCTGATGATTG 1440
QY 3049 ACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3108
Db 1441 ACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 3109 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3168
Db 1501 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 3169 CCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3228
Db 1561 CCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 3229 AATTTCAGATCTTTTATATGATGATGATGATGATGATGATGATGATGATGATGATG 3288
Db 1621 AATTTCAGATCTTTTATATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 3289 CAAATATACCCACACTTTGTTTATGATGATGATGATGATGATGATGATGATGATGATG 3325
Db 1681 CAAATATACCCACACTTTGTTTATGATGATGATGATGATGATGATGATGATGATGATG 1717

RESULT 9
ID ABV23150 standard; cDNA: 1299 Bp.
XX ABV23150;
XX AC
XX DT
XX DE 16-SEP-2002 (first entry)
XX KW Human prostate expression marker cDNA 23141.
XX OS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX PN pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200106860-A2.
XX PD 23-AUG-2001.
XX PE 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX

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Identifying agents for treating tumours and autoimmune disease -  
 Claim 3; Page 72-74; 85pp; French.  
 The present sequence encodes a human protein expressed in tumour cells.  
 The polynucleotide is useful for screening cDNA/genomic DNA banks and  
 for cloning isolated DNA; identifying mutant forms of the gene that  
 encodes a human protein, where the mutations are associated with  
 abnormal gene expression, or promoters and regulators of the gene,  
 particularly for diagnosis; for recombinant expression of the derived  
 protein; as probes and primers for detection and amplification; and  
 as antisense therapeutics. The tumour expressed protein is useful for  
 raising specific antibodies and to screen agents that modulate its  
 activity, bind to it or interact with it. These agents are potentially  
 useful for treatment or prevention of diseases associated with abnormal  
 expression/activity of the protein, particularly immunological diseases  
 (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic  
 infections.

Sequence 1149 BP; 308 A; 315 C; 277 G; 249 T; 0 other;

Query Match 34.4%; Score 1145.8; DB 22; Length 1149;  
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1147; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 463 AGCCTTCAGCCACATGAGAGCTGATGACAGTGTCTGAGTCCACCGGAAGTGTACT 522  
 Db 1 AGCCTTCAGCCACATGAGAGCTGATGACAGTGTCTGAGTCCACCGGAAGTGTACT 60  
 QY 523 TCGTCCAAAGTGGTTCCTCCCGGGGCGACATCATCGCTTCAACAGGAGCAATGCAAGCC 582  
 Db 61 TCGTCCAAAGTGGTTCCTCCCGGGGCGACATCATCGCTTCAACAGGAGCAATGCAAGCC 120  
 QY 583 ACACGTGATGAGCGCCGTGAACCTGAGCAATGTGGCACTGCACTGAAATGACTACT 642  
 Db 121 ACACGTGATGAGCGCCGTGAACCTGAGCAATGTGGCACTGCACTGAAATGACTACT 180  
 QY 643 CCAGACTCCAGCATCATCTTTGAGTTCCTGTTCAAGTACAGCAGTGCAGCCCAATGCA 702  
 Db 181 CCAGACTCCAGCATCATCTTTGAGTTCCTGTTCAAGTACAGCAGTGCAGCCCAATGCA 240  
 QY 703 GATGACTCCAGTGGATGAAGACACAGAGAAAGATGGGAATTCACAGTGTGAGCTA 762  
 Db 241 GATGACTCCAGTGGATGAAGACACAGAGAAAGATGGGAATTCACAGTGTGAGCTA 300  
 QY 763 AATGAGGCAATTAATGTCTCTAATGGAGAACACAGCCCTCTCGATGAGCAAGTA 822  
 Db 301 AATGAGGCAATTAATGTCTCTAATGGAGAACACAGCCCTCTCGATGAGCAAGTA 360  
 QY 823 CCCAAGCCTGTGTGGTGAAGAACTTCATTAACAGGGGTGGCTTACACTTCAGAAATGC 882  
 Db 361 CCCAAGCCTGTGTGGTGAAGAACTTCATTAACAGGGGTGGCTTACACTTCAGAAATGC 420  
 QY 883 TTCCCTCCCAAACTGGAGCATGATGACAAAGAGGCTCTCTTTTTCGAACTTTGTC 942  
 Db 421 TTCCCTCCCAAACTGGAGCATGATGACAAAGAGGCTCTCTTTTTCGAACTTTGTC 480  
 QY 943 CCAGCCAACTTATATTCATAAATAAGAGAACTTCTGCCACAGTGTGACCTGACAAA 1002  
 Db 481 CCAGCCAACTTATATTCATAAATAAGAGAACTTCTGCCACAGTGTGACCTGACAAA 540  
 QY 1003 TACTGAGAAAGAGATCTTCTCTGTAAGTGGGCCAGCTTGACAGACAAAGATTAT 1062  
 Db 541 TACTGAGAAAGAGATCTTCTCTGTAAGTGGGCCAGCTTGACAGACAAAGATTAT 600  
 QY 1063 TTCTACACACACAGGCGCTGGATGCCAAGGAGAGACACAACTCATATGTAATGGGCC 1122  
 Db 601 TTCTACACACACAGGCGCTGGATGCCAAGGAGAGACACAACTCATATGTAATGGGCC 660  
 QY 1123 AAGCCGAAATCTGTAGGAGACCTTGAGGGGAGTGAAGTGCCTGCTGGTGTG 1182  
 Db 661 AAGCCGAAATCTGTAGGAGACCTTGAGGGGAGTGAAGTGCCTGCTGGTGTG 720

QY 1183 AAGACCCAGTGGCCACCCTGCAACCCAGGCTTCTTCAAAAACCAACAGACACTGCCAG 1242  
 Db 721 AAGACCCAGTGGCCACCCTGCAACCCAGGCTTCTTCAAAAACCAACAGACACTGCCAG 780  
 QY 1243 CCCTGCGCATATGTTCTTCTACTTCAATGGCTCAGACTGTACCCGCTGCCGAGGACT 1302  
 Db 781 CCCTGCGCATATGTTCTTCTACTTCAATGGCTCAGACTGTACCCGCTGCCGAGGACT 840  
 QY 1303 GAACCCGCTGGGATTTGAATTAACAATGTTGGAGACAGCTGCCCAAAACATGAAAG 1362  
 Db 841 GAACCCGCTGGGATTTGAATTAACAATGTTGGAGACAGCTGCCCAAAACATGAAAG 900  
 QY 1363 ACCGTTCTAGTGGAGTCAACTTCAGATCAAGGGCATGACAGGCTGGAGGTGGCTGT 1422  
 Db 901 ACCGTTCTAGTGGAGTCAACTTCAGATCAAGGGCATGACAGGCTGGAGGTGGCTGT 960  
 QY 1423 GATCACAATTTACACAGCTGCTGGAGCTTACAGCAATGACTTCAATTTCACTGTGTT 1482  
 Db 961 GATCACAATTTACACAGCTGCTGGAGCTTACAGCAATGACTTCAATTTCACTGTGTT 1020  
 QY 1483 GTGCCGAGATTTAGACCTCCGAGTGGATGGAGGACAGACAGAGAAATAAGGTGGCC 1542  
 Db 1021 GTGCCGAGATTTAGACCTCCGAGTGGATGGAGGACAGACAGAGAAATAAGGTGGCC 1080  
 QY 1543 AGAATCACATTTGTCTTTGAGACCCCTGTCTGTTGAACTGTGAGCTTCACTTATGTG 1602  
 Db 1081 AGAATCACATTTGTCTTTGAGACCCCTGTCTGTTGAACTGTGAGCTTCACTTATGTG 1140  
 QY 1603 GGTGTGAAT 1611  
 Db 1141 GGTGTGAAT 1149

# RESULT 12

AAH76195  
 ID AAH76195 standard; cDNA; 1587 BP.

AC AAH76195;

PT 29-OCT-2001 (first entry)

XX Human seven-transmembrane protein 50288 cDNA sequence.

XX seven-transmembrane protein; G-protein coupled receptor; GPCR; human;

KW 17724; 50288; 31945; antiinflammatory; antiulcer; cytoskeletal; virulide;

KW hepatotropic; immunosuppressive; gynecological; neuroprotective; cardiant;

KW anti-HIV; immunostimulant; dermatological; antidiatherosclerotic; hemostatic;

KW antianemic; antiParkinsonian; nephrotropic; antithyroid; hemostatic;

KW cerebroprotective; osteopathic; analgesic; gene therapy; nootropic; ss.

OS Homo sapiens.

XX key

XX location/Qualifiers

XX CDS 308..1427

XX /\*tag= a

XX /product= "50288 protein"

XX WO200159117-A2.

XX 16-AUG-2001.

XX 12-FEB-2001; 2001WO-US04536.

XX 11-FEB-2000; 2000US-0182061.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA, Silos-Santiago I;

XX WPI: 2001-514670/56.

XX P-PSDB: AAB85768.

XX New seven-transmembrane protein/6-protein coupled receptor polypeptides





QY 2331 GCCCTGACGCTTGGTATGACCTATTTGGGGTGACAGATATGACTTGGATGAAAT 2390  
 DB 2325 ATCCATCTTCTGGCAGATACATTTATGAGATCAGACTTGAACACATTTGAAAAATAT 2384  
 QY 2391 CACCTCCAGAGTACATTTTCCACCTGAGATCCCTTGGGATFACCGAGCTGATCTTCTT 2450  
 DB 2385 TAATATTAAGAGATATGATTTCCAGTTCCAAAGCCAAATFACAGATGTGCAATTTCTT 2444  
 QY 2451 TTATAGTCCAAATGATGATGACCACTGCTGCAAGTTCTGGGATFACCAACCATCCGCGT 2510  
 DB 2445 TTATAGTCTTCTACAGCAACAACATCTTATTTATGAGCCGATCAACCTGCTGAAAAAT 2504  
 QY 2511 CAGGTGACAGTCCACAGAAAATCTGCTGCAAGTTGCTGCTGCAAGCAAGTCTGCTGCA 2570  
 DB 2505 GAGGTGATCTCTACTAATATCTGAGAGAGATTTTCACTCCCAAGCAAGTCCGCGC 2554  
 QY 2571 TGGGACCTGATGATGCTCAACTTCCACTTCTGCTGAGGAGCGCGGCTGCTGCGCT 2630  
 DB 2565 AGGTACCTGTGATGATGCTGATCTTCTATTTCTGAGGAGATGCTGAGAGCTTGCCTCT 2624  
 QY 2631 CTGCTGATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2690  
 DB 2625 GTGTACGGGACATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2684  
 QY 2691 TACTTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2750  
 DB 2685 CTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2744  
 QY 2751 AGTACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2810  
 DB 2745 GTTGGCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2804  
 QY 2811 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2870  
 DB 2805 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2864  
 QY 2871 GATACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2930  
 DB 2865 ATACAAATATTTCCAAAGTTATGATGATGATGATGATGATGATGATGATGATGATG 2924  
 QY 2931 TGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2989  
 DB 2925 AGACAGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2984  
 QY 2990 ACAAATCTCTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3049  
 DB 2985 ACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3044  
 QY 3050 CTCAGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3070  
 DB 3045 ATCTGTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3065  
 RESULT 14  
 AAH76196  
 ID AAH76196 standard: cDNA: 1119 BP.  
 AC AAH76196;  
 DE 29-OCT-2001 (first entry)  
 XX Human seven-transmembrane protein 50288 coding sequence.  
 XX  
 XX seven-transmembrane protein: G-protein coupled receptor; GPCR; human;  
 KW 17724; 50288; 31945; antiinflammatory; antileuk; cytosolic; virucide;  
 KW hepatotropic; immunosuppressive; gynecological; neuroprotective;  
 KW anti-HIV; immunostimulant; dermatological; antithrombotic; cardiant;  
 KW antianemic; antiparkinsonian; nephrotropic; antithyroid; hemostatic;  
 KW cerebroprotective; osteopathic; analgesic; gene therapy; nootropic; ss.  
 XX  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT CDS 1..1119  
 FT /tag- a  
 FT /product- "50288 protein"  
 XX  
 PN WO200159117-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 12-FEB-2001; 2001MO-US04536.  
 XX  
 PR 11-FEB-2000; 2000US-0182061.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Glucksmann MA, Slios-Santiago I;  
 XX  
 DR WPI: 2001-514670/56.  
 XX P-PSDB; AAB85678.  
 XX  
 PT New seven-transmembrane protein/G-protein coupled receptor polypeptides  
 PT and polynucleotides for diagnosing, treating seven-transmembrane  
 PT protein/receptor-related disorders and to identify modulators of  
 PT therapeutic use  
 XX  
 PS Claim 2; Page 142; 144pp; English.  
 XX  
 CC The invention provides isolated seven-transmembrane protein/G-protein  
 CC coupled receptor polypeptides selected from 17724, 50288, 31945 proteins.  
 CC The polypeptides can be expressed by standard recombinant methodology.  
 CC Modulators of the polypeptides can be identified using a competition  
 CC binding assay or an assay for receptor-mediated signal transduction. The  
 CC polypeptides and polynucleotides are useful as reagents or targets in  
 CC seven-transmembrane protein/receptor assays applicable to treatment and  
 CC diagnosis of seven-transmembrane protein/receptor mediated disorders  
 CC (see AAH76191 for a detailed description of the various disorders that  
 CC can be treated or diagnosed using the polypeptides). The polynucleotides  
 CC are useful to detect mutations in genes and gene expression products such  
 CC as mRNA, as antisense constructs to control gene expression and for  
 CC chromosome identification. The present sequence represents the human  
 CC seven transmembrane protein 50288 coding sequence.  
 CC  
 SQ Sequence 1119 BP; 275 A; 314 C; 296 G; 234 T; 0 other;  
 Query Match 28.5%; Score 951.8; DB 22; Length 1119;  
 Best Local Similarity 99.3%; Pred. No. 6.6e-271;  
 Matches 956; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 58 ATGCTGAGCTTGGGACAGACCAATCTCCGCAAGATGATGATGATGATGATGATGATGATG 117  
 DB 1 ATGCTGAGCTTGGGACAGACCAATCTCCGCAAGATGATGATGATGATGATGATGATGATG 60  
 QY 118 CGCATACCCGGCTGTGGGCTGTGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 177  
 DB 61 CGCATACCCGGCTGTGGGCTGTGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 120  
 QY 178 GGAACGGGACCGGAGCTTCAAGGCTGCAAGAGCTGATGATGATGATGATGATGATGATGATG 237  
 DB 121 GGAACGGGACCGGAGCTTCAAGGCTGCAAGAGCTGATGATGATGATGATGATGATGATGATG 180  
 QY 238 TGTGACAGCAGCGGCTTCCAGGTGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 297  
 DB 181 TGTGACAGCAGCGGCTTCCAGGTGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 240  
 QY 298 AGCTGCTGACCCCGCTCAAGGAGCAGGAGTCTCTTCTCTGCAACGCGGGGAGTTT 357  
 DB 241 AGCTGCTGACCCCGCTCAAGGAGCAGGAGTCTCTTCTCTGCAACGCGGGGAGTTT 300  
 QY 358 CTGATATGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417  
 DB 301 CTGATATGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 QY 418 GGCATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477





Db 891 ATTTCAGCAACAAACAGGTTCACTGACGCGAGGTGTGTCACAAACACCTATCTTGA 950  
 Qy 963 TAAAGAGAACTCTTGCCACCACTGTGACCTGTACAATAATCTGAGAAAGATCTTC 1022  
 Db 951 GAAAGAGCAAAAGATATATAGGTGTA--AGACGACTCTCAATTTTCAGATCCAG 1007  
 Qy 1023 TTCCTGTAACGTCGCGCCAGCTTGACAGAGCAAGATATTTCTTACACACACGCGCTG 1082  
 Db 1008 TAGGTGTACAGAGCGCCCTCCCTGTACCAACAAAGATATTTTCAGATCCACTCCATG 1067  
 Qy 1083 CGATGCCAAGAGAGACACAACTATGTACAAATGGCCCAAGCCGAATCTGTAGCGA 1142  
 Db 1068 TGATGAGAGAGAAAGACACATATATGTACAGGTGATAGAGCCCAAAATCTGCGGGA 1127  
 Qy 1143 GGACCTTGAGGGGCGATGAGAGCTGCGCTGTGTGTGAAGACCACTGCCACCTG 1202  
 Db 1128 GGATCTCACAGATGCTATATAGATGCCCCCTTGTGAGAGAAAGATTTGTCGCCCTTG 1187  
 Qy 1203 GAACCGAGCTTCTTCAAAACCAACAGACACGCGCGCCGCTGATATGTTCTTA 1262  
 Db 1188 CAACCGTGGATTTTATACAAATGATCATCTTTCGCACTCCCTGCTCGGAACAT 1247  
 Qy 1263 CTCCAAATG--CTCAGACTGTACCCGCTGCGCTGACAGGACTGAACCTGTGTGAT 1319  
 Db 1248 TTCAGATGAGAACCAAGATATGTAGACATGTCCACAGAGAGCGCTGCACTTGCTT 1307  
 Qy 1320 TGAATPACAAATGTGTGAACACGCTGCCCAACAAATGGAACGACGTTCTCATGGGAT 1379  
 Db 1308 TGAATATATAATGTGAATGTCTCCGCGCAACATGAAACCTCTCTCAATGTTGG 1367  
 Qy 1380 CAACCTCGATKCAAGGCACTACAGGCTGGAGGTGGCTGTGATCATTTTACACAGC 1439  
 Db 1368 GAATTCAAAGTCCGATGATGAATGATGGAGGTGCTGTGATCATTCACAGAGG 1427  
 Qy 1440 TCTGTGAGCTTCAGCAATGATCTTCTGATCTCTGCTGCTGCGAGATTTAGAC 1499  
 Db 1428 GGCTGAGGTTCTGACATGATTAATCTGATCTTAACTTGCTATCCAGATTTTAAAC 1487  
 Qy 1500 TCCGAGTGTGTATGGACACAGAGAAATGAAGGTGGCCAGAAATCAGATTTGTCT 1559  
 Db 1488 ACCAATATATGACTGTGGAGCCAC--GGGTCTGAACTAGAGAAATTAACATTTGCTT 1544  
 Qy 1560 TGAAGACCTCTGTCTGTGAATCTGTGAGCTCTACTTCAATGGGTGTGAATTTAGAGAC 1619  
 Db 1545 TGAGACCTCTGTGAGTACTGTGTTTGTACTTCAATGGGTGATTAATGAAGAAAG 1604  
 Qy 1620 CAACCTCTGTGAGAGCTGGAAGGTTTCCAAAGCAACAGCTCTTACTACTATCAT 1679  
 Db 1605 TACAAATGTGTAGATCTGTGGGTGGAACCAAGAAACAAAGCTTACACCATATCAT 1664  
 Qy 1680 TGAAGAGAACTATCACAGAGCTTCACTGGGCTTCCAGAGAGCACTTTTCATGAGGC 1739  
 Db 1665 CTTCAGAAATGCACTTTTACATTTTACATGGGCAATTCAGAGAGGTCAGAGA 1724  
 Qy 1740 AAGCAGAGATACCAATGAGCTTGCACAAAGATCTATCCATCATGTACACCAATGTAT 1799  
 Db 1725 TATATAGCGTTTATCATGATGATGTAAGATTTATTTCTATCAACAGCCACTAAAGCAGT 1784  
 Qy 1800 GATGCGCTGGCTCTACTAGCTGCGCTGCTGCTGCTTACAGAGCTTGTATGGGTCTCC 1859  
 Db 1785 TGATGGGTGGGTCTCTATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1844  
 Qy 1860 CTGCACTCTTGTCTGCTGTGTACTATATGACCGAGATTCAGAACCTGCGACTCTCG 1919  
 Db 1845 GTGTGTCCCTCTCCAGGCGCTACATGAGAAAGAAACCAACAGTCGAAAGATG 1904  
 Qy 1920 CCCCCCTAACAAATCTGAAAGCCACCGCTTATGTTGCGCAGGCTGTGTGCGCTG 1979  
 Db 1905 TCCACCTGACCTTACCTGTCCATATCAGGTATGTGCAAGAGGCTTGTATTCATG 1964  
 Qy 1980 TGTTCAGGAGCAAGAACACAGATCCTCTGTGCTACAAATGATTTGACCTTCTC 2039

Db 1965 CGGCGCTGGAGTAAAAACATCAGACCATTCGTTTGGCTATATGATGCTTTTCTA 2024  
 Qy 2040 ACGCAACATCCAAACAGACTTCACTACACTTCTCCGCTTGTGGCAACACCGTCAC 2099  
 Db 2025 CCATGAAAGAAAGAAATCAGATTTTGTGCACTATGACTTTAGAACCTCAGCGTGTGGCTC 2084  
 Qy 2100 TCTTGTGAGGGGCAAGCTTCACTTCCAAAGGTTGAAATTTACTTCCATCTTAACCT 2159  
 Db 2085 ATATATATATGCCCCAGCTTCACTCCTCAAGAGACAAATTTACTTCATTTCTTCATAT 2144  
 Qy 2160 CAGTCTCTGTGGAACCAAGGATGAGAAATGTCTGTGTGACCGACAAATGCTCAGACT 2219  
 Db 2145 CAGTTTATGTGGCATGAGGGAAGATGCGCTCTGTACCAACAAATATACAGACT 2204  
 Qy 2220 CCGATTTCTGAGGCTGATGAGGTT-----CTCAATCTATCAGACCTTACGT 2270  
 Db 2205 TACAGTAAAGAAATATGTGCGAGGCTAGATGATTAACAAATTTGGTAGGCGCATTTGT 2264  
 Qy 2271 CTGCGAGGCAAGTCATCCCGCCAGAGGTGACAGGCTTACAAAGCCGCGGTTCTCACA 2330  
 Db 2265 ATGCGAGTCAACAAATTTCTCTGTGAAAGTGAAGGTTTCCGAGACCTTATCATCACA 2324  
 Qy 2331 GCTGTGAGCGCTTGTGATGACTTATTTGGGTGACAAAGATATGACTCTGATGGAAT 2390  
 Db 2325 ATCCATCTTCTGCGAGATACATTCATATGAGATCAGAGTTGAACCAATTTGAAATAAT 2384  
 Qy 2391 CACCTCCCGAGCTGACTTTTCCACTGAGTCTCTTGGGATACCGGAGCTGATCTTCT 2450  
 Db 2385 TAAATPAAAGAAATATGTTTCCAGTTCACAAAGCCAAATACAGATGTGATTTCTT 2444  
 Qy 2451 TTAATGTTCAAGATGATGACCCAGCTCAGTCTGGGAGATTCACACATTCGCGCT 2510  
 Db 2445 TTAATAGCTTCTTACACAAACACATCTTATTAATGAGCGCATCACTGTGTGAAT 2504  
 Qy 2511 CAGGTGACGTCCACAGAAACCTGCTCGGAAGTTTGTCTGCTCCAGAGACGTCTCAGA 2570  
 Db 2505 GAGGTATATCTTCTAATCTGAGAGAGATTTTACGTCCACAGCAAGTGGCCAG 2564  
 Qy 2571 TGGAGCTGTATGCTGCAACTTCCACTTCTGTGTGGAAGAGCGGCTGCTTCCGCT 2630  
 Db 2565 AGGTACCTGTATGCTGTGATGCTTCTTCTGTGTGGAAGAGTGTCAACCTTCCCTCT 2624  
 Qy 2631 CTGCTCACTGAGTACATACATGCTATCGTACAGAGCTGTGTGCTGGATCCAGAAAG 2690  
 Db 2625 GTTACGAGAGATGACTTCCATGATTTGAGAGAGCTGCAAGAGAGATTTAGAGAAC 2684  
 Qy 2691 TACTTACGTGTGGAGAACCAAGCTATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2750  
 Db 2685 CTGTATGTGTGGAATGAACTTAATGTGTCAATTAAGAAATTTCTTGTGCTGAGAAAA 2744  
 Qy 2751 AGTACCATCTGCAAAACATAGATTTCTGTGTGGAAGTGGCATCTGTGAGGACCTG 2810  
 Db 2745 GTTGGCAACCTGTGAAACGCTTGTGTGGAAGTGGAGCGGTGTGGAGCTTCTT 2804  
 Qy 2811 TACTGCACTCTGCTCAACCTGCTGACCTGCTCTTGTGGAAGAAAGATCAAAATCTAG 2870  
 Db 2805 TACTGCGCTTGT 2864  
 Qy 2871 GTACAAATCTCCAAAGCTGTGA 2893  
 Db 2865 GAAGACCATTTTGAATCTGTCA 2887

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 Job time : 517 secs

